The sequence of the \textit{trp} operon of \textit{Bacillus subtilis} 168 (\textit{trpC2}) revisited

The complete genome sequence of \textit{Bacillus subtilis} has been published (4) and is available at the \textit{SubtiList} site (http://www.pasteur.fr/Bio/SubtiList/).

The more mindful and curious readers were probably surprised by the absence of any detectable defect in the sequence of the \textit{trpC} cistron, despite the well known tryptophan requirement of \textit{B. subtilis} 168, the laboratory strain of choice due to its amenability to genetic analysis (hereafter designated 168 \textit{trpC}). In fact, the deposited sequence of the \textit{trp} operon was derived from the one published by Henner \textit{et al.} (3) performed on strain W168, a prototrophic derivative of \textit{B. subtilis} 168 (\textit{trpC2}). The two \textit{Ile} residues (110–111 in \textit{B. subtilis}, 117–118 in the \textit{E. coli} enzyme) are at the junction of the \textit{B} strand and \textit{C} helix and not directly involved in the formation of the active site of the enzyme. Nevertheless, they are near two invariant residues (Lys114 and Phe116 in \textit{E. coli}, Lys107 and Phe109 in \textit{B. subtilis}) involved in the active site: the deletion of one of the hydrophobic residues could interfere with the formation of the hydrophobic pocket or with the correct positioning of the phosphate-binding site, thus explaining the reported complete absence of enzyme activity (1).

\textbf{Alessandra M. Albertini* and Alessandro Galizzi}

Dipartimento di Genetica e Microbiologia, Università degli Studi di Pavia, 1 via Ferrata, 1-27100 Pavia, Italy

*For correspondence.

Tel: +39 0382 505549. Fax: +39 0382 528496. e-mail: albert@pillo.unipv.it

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Communications should be in the form of letters and should be brief and to the point. A single small Table or Figure may be included, as may a limited number of references (cited in the text by numbers, and listed in alphabetical order at the end of the letter). A short title (fewer than 50 characters) should be provided.

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